

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/357,375

DATE: 05/12/2000  
TIME: 14:24:30

INPUT SET: S35473.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: ARTHUR, MICHEL  
DUKTA-MALEN, SYLVIE  
MOLINAS, CATHERINE  
COURVALIN, PATRICE

ENTERED

(ii) TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE  
EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR  
IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR  
THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
(B) STREET: 1755 S. Jefferson Davis Highway, Suite 400  
(C) CITY: Arlington  
(D) STATE: Virginia  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22202

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/357,375  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/286,819  
(B) FILING DATE: 05-AUG-1994

(A) APPLICATION NUMBER: US 08/174,682  
(B) FILING DATE: 28-DEC-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/917,146

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/357,375DATE: 05/12/2000  
TIME: 14:24:30

INPUT SET: S35473.raw

47 (B) FILING DATE: 10-AUG-1992  
48  
49  
50 (vii) PRIOR APPLICATION DATA:  
51 (A) APPLICATION NUMBER: PCT/FR/91/00855  
52 (B) FILING DATE: 29-OCT-1991  
53  
54 (vii) PRIOR APPLICATION DATA:  
55 (A) APPLICATION NUMBER: FR 9013579  
56 (B) FILING DATE: 31-OCT-1990  
57  
58  
59 (viii) ATTORNEY/AGENT INFORMATION:  
60 (A) NAME: Oblon, Norman F.  
61 (B) REGISTRATION NUMBER: 24,618  
62 (C) REFERENCE/DOCKET NUMBER: 660-060-0 PCT  
63  
64 (ix) TELECOMMUNICATION INFORMATION:  
65 (A) TELEPHONE: (703) 413-3000  
66 (B) TELEFAX: (703) 413-2220  
67 (C) TELEX: 248855 OPAT UR  
68  
69 (2) INFORMATION FOR SEQ ID NO:1:  
70  
71 (i) SEQUENCE CHARACTERISTICS:  
72 (A) LENGTH: 966 base pairs  
73 (B) TYPE: nucleic acid  
74 (C) STRANDEDNESS: unknown  
75 (D) TOPOLOGY: linear  
76  
77 (ii) MOLECULE TYPE: DNA (genomic)  
78  
79  
80 (ix) FEATURE:  
81 (A) NAME/KEY: CDS  
82 (B) LOCATION: 1..966  
83  
84  
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
86  
87 ATG AAT AAC ATC GGC ATT ACT GTT TAT GGA TGT GAG CAG GAT GAG GCA 48  
88 Met Asn Asn Ile Gly Ile Thr Val Tyr Gly Cys Glu Gln Asp Glu Ala  
89 1 5 10 15  
90  
91 GAT GCA TTC CAT GCT CTT TCG CCT CGC TTT GGC GTT ATG GCA ACG ATA 96  
92 Asp Ala Phe His Ala Leu Ser Pro Arg Phe Gly Val Met Ala Thr Ile  
93 20 25 30  
94  
95 ATT AAC GCC AAC GTG TCG GAA TCC AAC GCC AAA TCC GCG CCT TTC AAT 144  
96 Ile Asn Ala Asn Val Ser Glu Ser Asn Ala Lys Ser Ala Pro Phe Asn  
97 35 40 45  
98  
99 CAA TGT ATC AGT GTG GGA CAT AAA TCA GAG ATT TCC GCC TCT ATT CTT 192

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/357,375

DATE: 05/12/2000

TIME: 14:24:30

INPUT SET: S35473.raw

100	Gln Cys Ile Ser Val Gly His Lys Ser Glu Ile Ser Ala Ser Ile Leu	
101	50 55 60	
102		
103	CTT GCG CTG AAG AGA GCC GGT GTG AAA TAT ATT TCT ACC CGA AGC ATC	240
104	Leu Ala Leu Lys Arg Ala Gly Val Lys Tyr Ile Ser Thr Arg Ser Ile	
105	65 70 75 80	
106		
107	GGC TGC AAT CAT ATA GAT ACA ACT GCT GCT AAG AGA ATG GGC ATC ACT	288
108	Gly Cys Asn His Ile Asp Thr Thr Ala Ala Lys Arg Met Gly Ile Thr	
109	85 90 95	
110		
111	GTC GAC AAT GTG GCG TAC TCG CCG GAT AGC GTT GCC GAT TAT ACT ATG	336
112	Val Asp Asn Val Ala Tyr Ser Pro Asp Ser Val Ala Asp Tyr Thr Met	
113	100 105 110	
114		
115	ATG CTA ATT CTT ATG GCA GTA CGC AAC GTA AAA TCG ATT GTG CGC TCT	384
116	Met Leu Ile Leu Met Ala Val Arg Asn Val Lys Ser Ile Val Arg Ser	
117	115 120 125	
118		
119	GTG GAA AAA CAT GAT TTC AGG TTG GAC AGC GAC CGT GGC AAG GTA CTC	432
120	Val Glu Lys His Asp Phe Arg Leu Asp Ser Asp Arg Gly Lys Val Leu	
121	130 135 140	
122		
123	AGC GAC ATG ACA GTT GGT GTG GTG GGA ACG GGC CAG ATA GGC AAA GCG	480
124	Ser Asp Met Thr Val Gly Val Val Gly Thr Gly Gln Ile Gly Lys Ala	
125	145 150 155 160	
126		
127	GTT ATT GAG CGG CTG CGA GGA TTT GGA TGT AAA GTG TTG GCT TAT AGT	528
128	Val Ile Glu Arg Leu Arg Gly Phe Gly Cys Lys Val Leu Ala Tyr Ser	
129	165 170 175	
130		
131	CGC AGC CGA AGT ATA GAG GTA AAC TAT GTA CCG TTT GAT GAG TTG CTG	576
132	Arg Ser Arg Ser Ile Glu Val Asn Tyr Val Pro Phe Asp Glu Leu Leu	
133	180 185 190	
134		
135	CAA AAT AGC GAT ATC GTT ACG CTT CAT GTG CCG CTC AAT ACG GAT ACG	624
136	Gln Asn Ser Asp Ile Val Thr Leu His Val Pro Leu Asn Thr Asp Thr	
137	195 200 205	
138		
139	CAC TAT ATT ATC AGC CAC GAA CAA ATA CAG AGA ATG AAG CAA GGA GCA	672
140	His Tyr Ile Ile Ser His Glu Gln Ile Gln Arg Met Lys Gln Gly Ala	
141	210 215 220	
142		
143	TTT CTT ATC AAT ACT GGG CGC GGT CCA CTT GTA GAT ACC TAT GAG TTG	720
144	Phe Leu Ile Asn Thr Gly Arg Gly Pro Leu Val Asp Thr Tyr Glu Leu	
145	225 230 235 240	
146		
147	GTT AAA GCA TTA GAA AAC GGG AAA CTG GGC GGT GCC GCA TTG GAT GTA	768
148	Val Lys Ala Leu Glu Asn Gly Lys Leu Gly Gly Ala Ala Leu Asp Val	
149	245 250 255	
150		
151	TTG GAA GGA GAG GAA GAG TTT TTC TAC TCT GAT TGC ACC CAA AAA CCA	816
152	Leu Glu Gly Glu Glu Glu Phe Phe Tyr Ser Asp Cys Thr Gln Lys Pro	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/357,375

DATE: 05/12/2000  
TIME: 14:24:31

INPUT SET: S35473.raw

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153          260          265          270
154
155  ATT GAT AAT CAA TTT TTA CTT AAA CTT CAA AGA ATG CCT AAC GTG ATA      864
156  Ile Asp Asn Gln Phe Leu Leu Lys Leu Gln Arg Met Pro Asn Val Ile
157          275          280          285
158
159  ATC ACA CCG CAT ACG GCC TAT TAT ACC GAG CAA GCG TTG CGT GAT ACC      912
160  Ile Thr Pro His Thr Ala Tyr Tyr Thr Glu Gln Ala Leu Arg Asp Thr
161          290          295          300
162
163  GTT GAA AAA ACC ATT AAA AAC TGT TTG GAT TTT GAA AGG AGA CAG GAG      960
164  Val Glu Lys Thr Ile Lys Asn Cys Leu Asp Phe Glu Arg Arg Gln Glu
165  305          310          315          320
166
167  CAT GAA      966
168  His Glu
169
170
171
172  (2) INFORMATION FOR SEQ ID NO:2:
173
174      (i) SEQUENCE CHARACTERISTICS:
175          (A) LENGTH: 322 amino acids
176          (B) TYPE: amino acid
177          (D) TOPOLOGY: linear
178
179      (ii) MOLECULE TYPE: protein
180
181      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
182
183  Met Asn Asn Ile Gly Ile Thr Val Tyr Gly Cys Glu Gln Asp Glu Ala
184      1          5          10          15
185
186  Asp Ala Phe His Ala Leu Ser Pro Arg Phe Gly Val Met Ala Thr Ile
187          20          25          30
188
189  Ile Asn Ala Asn Val Ser Glu Ser Asn Ala Lys Ser Ala Pro Phe Asn
190          35          40          45
191
192  Gln Cys Ile Ser Val Gly His Lys Ser Glu Ile Ser Ala Ser Ile Leu
193          50          55          60
194
195  Leu Ala Leu Lys Arg Ala Gly Val Lys Tyr Ile Ser Thr Arg Ser Ile
196          65          70          75          80
197
198  Gly Cys Asn His Ile Asp Thr Thr Ala Ala Lys Arg Met Gly Ile Thr
199          85          90          95
200
201  Val Asp Asn Val Ala Tyr Ser Pro Asp Ser Val Ala Asp Tyr Thr Met
202          100          105          110
203
204  Met Leu Ile Leu Met Ala Val Arg Asn Val Lys Ser Ile Val Arg Ser
205          115          120          125

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**INPUT SET: S35473.raw**

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206
207 Val Glu Lys His Asp Phe Arg Leu Asp Ser Asp Arg Gly Lys Val Leu
208      130                      135                      140
209
210 Ser Asp Met Thr Val Gly Val Val Gly Thr Gly Gln Ile Gly Lys Ala
211 145      150                      155                      160
212
213 Val Ile Glu Arg Leu Arg Gly Phe Gly Cys Lys Val Leu Ala Tyr Ser
214      165                      170                      175
215
216 Arg Ser Arg Ser Ile Glu Val Asn Tyr Val Pro Phe Asp Glu Leu Leu
217      180                      185                      190
218
219 Gln Asn Ser Asp Ile Val Thr Leu His Val Pro Leu Asn Thr Asp Thr
220      195                      200                      205
221
222 His Tyr Ile Ile Ser His Glu Gln Ile Gln Arg Met Lys Gln Gly Ala
223      210                      215                      220
224
225 Phe Leu Ile Asn Thr Gly Arg Gly Pro Leu Val Asp Thr Tyr Glu Leu
226 225      230                      235                      240
227
228 Val Lys Ala Leu Glu Asn Gly Lys Leu Gly Gly Ala Ala Leu Asp Val
229      245                      250                      255
230
231 Leu Glu Gly Glu Glu Glu Phe Phe Tyr Ser Asp Cys Thr Gln Lys Pro
232      260                      265                      270
233
234 Ile Asp Asn Gln Phe Leu Leu Lys Leu Gln Arg Met Pro Asn Val Ile
235      275                      280                      285
236
237 Ile Thr Pro His Thr Ala Tyr Tyr Thr Glu Gln Ala Leu Arg Asp Thr
238      290                      295                      300
239
240 Val Glu Lys Thr Ile Lys Asn Cys Leu Asp Phe Glu Arg Arg Gln Glu
241 305      310                      315                      320
242
243 His Glu
244
245

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
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